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APR 2 7 7006 TRADEMAN

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SEQUENCE LISTING

<110> DARROW, ANDREW LAWRENCE QI, JIAN-SHEN CHEN, CAILIN ANDRADE-GORDON, PATRICIA <120> HUMAN PRSS11-LIKE S2 SERINE PROTEASE AND USES THEREOF <130> ORT-1644-CIP <140> 10/617,443 <141> 2003-07-02 <150> 10/189,099 <151> 2002-07-03 <160> 31 <170> PatentIn Ver. 3.3 <210> 1 <211> 3006 <212> DNA <213> Homo sapiens <400> 1 cagggacteg aagtttgcag teetecacae teagtteeca cagatgtggt aggaggeat 60 attcagtccc atttttcaga tgaggagttg aggcccagag aacgtaagta atctgtctga 120 ggccacacag ctagaaagca gccaggccca gccgaacccc tggtgtgtgc agcccccagc 180 ccagttgctc attgcggggc tcgggagcca cgagcgaggc tgagcagcat gtgttccaga 240 tggtgggaac tggagagagc ccggcacagg cccgtgcagg gaaccccgag ggctgtaggc 300 cccgtgccac tgcatgcctc aggcctgtgg tcctggcagc cacagcccct actgctgacg 360 gcagcaggaa tctgagcccg ggaagggtcc agggaagttc gtgaaccatc tagcaagtcg 420 ggctggggtg tggccaagtt agacacagat gtagggccct gtggactcag aaattggcag 480 ctcttttggc ccagaggggc cacgctgtgt ccgggcctgg gtagctcaga agggtcacct 540 gggggtcttc cactacaccc ccgcctggac actgctgtag ccccagggct cggagggacc 600 agctggagcc catgaggaga gggccagttc tctcctgtaa gggtattgct gtagcatgag 660 ggaacagaca aggcccaggg ggactaaccc gagatccagc cccggcctca ctcccgtgtg 720 gctcacggca atatcctaac ctctctctga gcctcctgcc cagcctagca gggtccagtg 780 aggggggtga ggaagcccag cacgtggaag cctttttaac cattctcggg gtgagcgagc 840 cccttcccaa atgcctggtg tcactgcact gctgtgtggt agggggtccc caacgggctc 900 agtgtgggct gaggctggct ctgaactggg acaggggtct caggaagagc ctcctcctcc 960 tgcccactgg gcataggcct ctgggagctg gcagcatcgt gatctcactg atgcacctgg 1020 cccttcccgc cagcgcaggt ctccaccagc tgagcagccc gcgctacaag ttcaacttca 1080 ttgctgacgt ggtggagaag atcgcaccag ccgtggtcca catagagctc ttcctgagac 1140 accegetgtt tggccgcaac gtgcccctgt ccageggttc tggcttcatc atgtcagagg 1200 ccggcctgat catcaccaat gcccacgtgg tgtccagcaa cagtgctgcc ccgggcaggc 1260 agcageteaa ggtgeageta cagaatgggg acteetatga ggeeaceate aaagaeateg 1320 acaagaagtc ggacattgcc accatcaaga tccatcccaa gaaaaagctc cctgtgttgt 1380 tgctgggtca ctcggccgac ctgcggcctg gggagtttgt ggtggccatc ggcagtccct 1440 tcgccctaca gaacacagtg acaacgggca tcgtcagcac tgcccagcgg gagggcaggg 1500 agetgggeet eegggaetee gacatggaet acateeagae ggatgeeate ateaactaeg 1560 ggaactccgg gggaccactg gtgaacctgg atggcgaggt cattggcatc aacacgctca 1620 aggtcacggc tggcatctcc tttgccatcc cctcagaccg catcacacgg ttcctcacag 1680 agttccaaga caagcagatc aaagactgga agaagcgctt catcggcata cggatgcgga 1740 cgatcacacc aagcctggtg gatgagctga aggccagcaa cccggacttc ccagaggtca 1800 gcagtggaat ttatgtgcaa gaggttgcgc cgaattcacc ttctcagaga ggcggcatcc 1860 aagatggtga catcatcgtc aaggtcaacg ggcgtcctct agtggactcg agtgagctgc 1920 aggaggccgt gctgaccgag tctcctctcc tactggaggt gcggcggggg aacgacgacc 1980 tectetteag categeacet gaggtggtea tgtgagggge geatteetee agegeeaage 2040 gtcagagcct gcagacaacg gagggcagcg cccccccgag atcaggacga aggaccaccg 2100 teggteetea geagggegge ageeteetee tggetgteeg gggeagageg gaggetggge 2160 ttggccaggg gcccgaattt ccgcctgggg agtgttggat ccacatcccg gtgccgggga 2220 gggaageeca acateeeett gtacagatga teetgaaagt caetteeaag tteteeggat 2280 atteacaaaa etgeetteea tggaggteee eteeteteet agetteeege etetgeeeet 2340 gtgaacaccc atctgcagta teceetgete etgeeeetee taetgeaggt etgggetgee 2400 aagettette eeceetgaca aaegeeeace tgaeetgagg eeceagette eetetgeeet 2460 aggacttacc aagctgtagg gccagggctg ctgcctgcca gcctggggtc cctggaggac 2520 aggtcacatc tgatcccttt ggggtgcggg ggtggggtcc agcccagagc aggcactgag 2580 tgaatgcccc ctggctgcgg agctgagccc cgccctgcca tgaggttttc ctccccaggc 2640 aggcaggagg ccgcggggag cacgtggaaa gttggctgct gcctggggaa gcttctcctc 2700 cccaaggegg ccatggggca gcctgcagag gacagtggac gtggagctgc ggggtgtgag 2760 gactgageeg getteeeett eecaegeage tetgggatge ageageeget egeatggaag 2820 tgccgcccag aggcatgcag gctgctgggc accacccct catccaggga acgagtgtgt 2880 ctcaaqqqqc atttgtgagc tttgctgtaa atggattccc agtgttgctt gtactgtatg 2940 aaaaaa

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Arg Asn Val Pro Leu Ser Ser Gly Ser Gly Phe Ile Met Ser Glu Ala 50 55 60

Gly Leu Ile Ile Thr Asn Ala His Val Val Ser Ser Asn Ser Ala Ala 65 70 75 80

Pro Gly Arg Gln Gln Leu Lys Val Gln Leu Gln Asn Gly Asp Ser Tyr 85 90 95

Glu Ala Thr Ile Lys Asp Ile Asp Lys Lys Ser Asp Ile Ala Thr Ile 100 105 110

Lys Ile His Pro Lys Lys Lys Leu Pro Val Leu Leu Gly His Ser 115 120 125

Ala Asp Leu Arg Pro Gly Glu Phe Val Val Ala Ile Gly Ser Pro Phe 130 135 140

Ala Leu Gln Asn Thr Val Thr Thr Gly Ile Val Ser Thr Ala Gln Arg 145 150 155 160

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Gln Asn Thr Val Thr Thr Gly Ile Val Ser Thr Thr Gln Arg Gly Gly

300

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Lys Glu Leu Gly Leu Arg Asn Ser Asp Met Asp Tyr Ile Gln Thr Asp 305 310 315 320

Ala Ile Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn Leu Asp 325 330 335

Gly Glu Val Ile Gly Ile Asn Thr Leu Lys Val Thr Ala Gly Ile Ser 340 345 350

Phe Ala Ile Pro Ser Asp Lys Ile Lys Lys Phe Leu Thr Glu Ser His 355 360 365

Asp Arg Gln Ala Lys Gly Lys Ala Ile Thr Lys Lys Lys Tyr Ile Gly 370 380

Ile Arg Met Met Ser Leu Thr Ser Ser Lys Ala Lys Glu Leu Lys Asp 385 390 395 400

Arg His Arg Asp Phe Pro Asp Val Ile Ser Gly Ala Tyr Ile Ile Glu 405 410 415

Val Ile Pro Asp Thr Pro Ala Glu Ala Gly Gly Leu Lys Glu Asn Asp 420 425 430

Val Ile Ile Ser Ile Asn Gly Gln Ser Val Val Ser Ala Asn Asp Val 435 440 445

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Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly 50 55 60

Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
65 70 75 80

Ala Gl
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Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
100 105 110

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- Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg 130 135 140
- Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala 145 150 155 160
- Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu 165 170 175
- Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu 180 185 190
- Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Val Arg Val
 195 200 205
- Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp 210 215 220
- Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu 225 230 235 235
- Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe 245 250 255
- Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser 260 265 270
- Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro 275 280 285
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- Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp 325 330 335
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- Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr 355 360 365
- Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe 370 375 380
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Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile 405 410 415

Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg 420 425 430

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Lys Ile Ala Pro Ala Val Val His Ile Glu Leu Phe Leu Arg His Pro 50 55 60

Leu Phe Gly Arg Asn Val Pro Leu Ser Ser Gly Ser Gly Phe Ile Met 65 70 75 80

Ser Glu Ala Gly Leu Ile Ile Thr Asn Ala His Val Val Ser Ser Asn 85 90 95

Ser Ala Ala Pro Gly Arg Gln Gln Leu Lys Val Gln Leu Gln Asn Gly
100 105 110

Asp Ser Tyr Glu Ala Thr Ile Lys Asp Ile Asp Lys Lys Ser Asp Ile 115 120 125

Ala Thr Ile Lys Ile His Pro Lys Lys Leu Pro Val Leu Leu Leu 130 135 140

Gly His Ser Ala Asp Leu Arg Pro Gly Glu Phe Val Val Ala Ile Gly 145 150 155 160

Ser Pro Phe Ala Leu Gln Asn Thr Val Thr Thr Gly Ile Val Ser Thr 165 170 175

Ala Gln Arg Glu Gly Arg Glu Leu Gly Leu Arg Asp Ser Asp Met Asp 180 185 190

Tyr Ile Gln Thr Asp Ala Ile Ile Asn Tyr Gly Asn Ser Gly Gly Pro 195 200 205

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